

IN THE SPECIFICATION:

Please add the following text as a separate paragraph immediately after the title of the invention in the specification:

This application claims the right of priority under 35 U.S.C. §119(a)-(d) to Japanese Patent Applications JP2001-053465 filed February 28, 2001 and JP2002-022682 filed January 31, 2002.

Please replace paragraph at page 18, line 3 through page 19, line 10, with the following amended paragraph:

Classification of genes into any among 11 to 19 is decided based on terminology defined in the ontology database constructed by the International Ontology Consortium (<http://www.geneontology.org>). Gene related ontology can be searched on PubGene (<http://www.pubgene.org>), which is one of publicly offered ontology database, or Gene Ontology (GO). The PubGene database connects gene with ontology through textual analysis of Medline, OMIM, etc. (refer to Tor-Kristian Jenssen et al. A literature network of human genes for high-throughput analysis of gene expression. *Nature Genetics*, vol.28, pp21-28). In PubGene classification, HSPA1A, for example, which is a heat shock protein (HSP), is closely associated with Heat shock protein (GO No. 0003773) in the Functional Annotation and with transcription (GO No. 006350) and immune response (GO No. 0006955) in the Cell Process Annotation. Another HSP, HSPA1B, is classified to Heat shock protein (GO No. 0003773) in the Functional Annotation and apoptosis (GO No. 0006915) in the Cell Process Annotation. Therefore, according to the Functional Annotation in PubGene, for example, both HSPA1A and HSPA1B belong to the same stress related gene, that is, heat stress protein. The two are classified to No. 12 Stress and survival-related genes and hormone genes. According to the Cell Process Annotation in PubGene, on the other hand, HSPA1A belongs to No. 13 Immune response related genes, and HSPA1B to No. 14 Apoptosis and cell death related genes. Ontology in the Functional Annotation and Cell Process Annotation in PubGene is listed in the order of scores. Therefore, ontology with the largest score or several numbers of ontology with relatively large scores are selected for classification. Along with PubGene, any tool or database can be used to search ontology based on gene names.

Please replace paragraph at page 22, lines 8-25, with the following amended paragraph:

Positioning based on the above (4) information on gene pathway means that genes related to intracellular and intercellular information transfer are positioned according to correlations in pathway. FIGURE 8 illustrates the typical pathway, that is, MAPK (mitogen activated protein kinase) pathway. Circles indicate genes, and arrows connecting genes indicated the directions of information transfer between genes. For example, positioning of MEK gene adjacent to Mos gene and positioning Raf gene and ERK gene adjacent to MEK gene demonstrate that these genes belong to the same pathway and genes that transfer information directly are positioned close to each other. Other pathway information, for example, Pathway database (<http://www.biocarta.com/>), can also be used. Gene positioning can also be reflected on compiled information related to gene relationship, such as metabolic pathway database KEGG (<http://www.kegg.kyoto.u.ac.jp>).

Please replace paragraph at page 51, lines 13-23, with the following amended paragraph:

From the total RNA or messenger RNA extracted from cells and tissues, cDNA is synthesized in transcription reaction originating at primer such as oligo-dT primer using transcription enzymes. At the DNA synthesis, for example, fluorescent labels are taken up by cDNA by adding to solution deoxynucleotides to which fluorescent dyes such as Cy3-dCTP, Cy3-dUTP, Cy5-dCTP and Cy5-dUTP are bound. By hybridizing the fluorescent-labeled cDNA with probes fixed on the DNA ~~chip~~ chip substrate, RNA profile of genes can be measured using the level of fluorescence.